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QY 121 WVINCFRHSFQYVDARHFEI FPNQIFKIGTDFGLTEFKWKFYSQFNKESAFITGY 180
  |||
DB 121 WVLNGFRHQSQYVDARHFEI FPNQIFKIGTDFGLTEFKWKFYSQFNKESAFITGY 180
QY 181 ATASWISQWSESPPVVASPGGAFPCVITFNESEAFKGIYYNQKHKSSKIYHTSPVKIDS 240
  |||
DB 181 ATASWISQWSESPPVVASPGGAFPCVITFNESEAFKGIYYNQKHKSSKIYHTSPVKIDS 240
QY 241 GPTAGKRMNIVNNVSSPFAWKYNPHVILSVAGIATFETVRLANKQYVIGVNSIQGM 300
  |||
DB 241 GPTAGKRMNIVNNVSSPFAWKYNPHVILSVAGIATFETVRLANKQYVIGVNSIQGM 300
QY 301 IQDQPIILSVLHFKQAVYETILMILEFTEDYFYVVFHFAFKWHSHELTAFKFWIG 360
  |||
DB 301 IQDQPIILSVLHFKQAVYETILMILEFTEDYFYVVFHFAFKWHSHELTAFKFWIG 360
QY 361 VARNHESNFEQAKINNKTEKATKMKELFEFEVAYINSKALEKQNKIDNVSRLEAI 420
  |||
DB 361 VARNHESNFEQAKINNKTEKATKMKELFEFEVAYINSKALEKQNKIDNVSRLEAI 420
QY 421 SAINKAAK 428
  |||
DB 421 SAINKAAK 428

RESULT 6
QYRNG PRELIMINARY: PRT: 428 AA.
AC QYRNG3
DT 01-MAY-2000 (TREMREL: 13, Created)
DT 01-MAY-2000 (TREMREL: 13, Last sequence update)
DT 01-JUN-2001 (TREMREL: 18, Last annotation update)
DE MACROPHAGE ACTIVATING LIPOPROTEIN-403 PRECURSOR.
GN MALP.
OS Mycoplasma fermentans.
OC Bacteria; Firmicutes; Bacillus/Clustidium group; Mollicutes.
MC Mycoplasmataceae; Mycoplasma.
CX NCBI_TaxID: 2115.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN P318, M39A, AND M70B;
RX MEDLINE 99115554; PubMed 9916088;
RA Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
RT "Differential posttranslational processing confers intraspecies
  variation of a major surface lipoprotein and a macrophage-activating
  lipopeptide of Mycoplasma fermentans.";
  EMBL: AF099215; AAD16397.1;
  FJ InterPro: IPR003760; Bmp.
  DR Pfam: PF02608; Bmp; 1.
  KW Signal; Lipoprotein.
  FT SIGNAL 1 24 POTENTIAL.
  FT CHAIN 25 38 MACROPHAGE ACTIVATING LIPOPROTEIN 403.
  SQ SEQUENCE 428 AA: 47843 MW: 59692.422 kDa pI: 5.64;

Query Match 99.48; Score 2174; DB 2; Length 428;
Best local Similarity 99.48; Pred. No. 10-117;
Matches 425; Conservative 1; Mismatches 0; Gaps 0;

QY 1 MKRSKKILLGLSPFAALLFAVAVSGNNNESNISSEKFIKSYTTINANGKQVKNNAELL 60
  |||
DB 1 MKRSKKILLGLSPFAALLFAVAVSGNNNESNISSEKFIKSYTTINANGKQVKNNAELL 60
QY 61 KLRVILIDCKIDKSFNSAFKALKAINKQTGIEIRNVTHSSNEFSAYNSALSAGHVI 120
  |||
DB 61 KLRVILIDCKIDKSFNSAFKALKAINKQTGIEIRNVTHSSNEFSAYNSALSAGHVI 120
QY 121 WVLNGFRHQSQYVDARHFEI FPNQIFKIGTDFGLTEFKWKFYSQFNKESAFITGY 180
  |||
DB 121 WVLNGFRHQSQYVDARHFEI FPNQIFKIGTDFGLTEFKWKFYSQFNKESAFITGY 180
QY 181 ATASWISQWSESPPVVASPGGAFPCVITFNESEAFKGIYYNQKHKSSKIYHTSPVKIDS 240
  |||
DB 181 ATASWISQWSESPPVVASPGGAFPCVITFNESEAFKGIYYNQKHKSSKIYHTSPVKIDS 240

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DB 121 WVINCFRHSFQYVDARHFEI FPNQIFKIGTDFGLTEFKWKFYSQFNKESAFITGY 180
QY 181 ATASWISQWSESPPVVASPGGAFPCVITFNESEAFKGIYYNQKHKSSKIYHTSPVKIDS 240
  |||
DB 181 ATASWISQWSESPPVVASPGGAFPCVITFNESEAFKGIYYNQKHKSSKIYHTSPVKIDS 240
QY 241 GPTAGKRMNIVNNVSSPFAWKYNPHVILSVAGIATFETVRLANKQYVIGVNSIQGM 300
  |||
DB 241 GPTAGKRMNIVNNVSSPFAWKYNPHVILSVAGIATFETVRLANKQYVIGVNSIQGM 300
QY 301 IQDQPIILSVLHFKQAVYETILMILEFTEDYFYVVFHFAFKWHSHELTAFKFWIG 360
  |||
DB 301 IQDQPIILSVLHFKQAVYETILMILEFTEDYFYVVFHFAFKWHSHELTAFKFWIG 360
QY 361 VARNHESNFEQAKINNKTEKATKMKELFEFEVAYINSKALEKQNKIDNVSRLEAI 420
  |||
DB 361 VARNHESNFEQAKINNKTEKATKMKELFEFEVAYINSKALEKQNKIDNVSRLEAI 420
QY 421 SAINKAAK 428
  |||
DB 421 SAINKAAK 428

RESULT 7
QYRNG PRELIMINARY: PRT: 428 AA.
AC QYRNG3
DT 01-MAY-2000 (TREMREL: 13, Created)
DT 01-MAY-2000 (TREMREL: 13, Last sequence update)
DT 01-JUN-2001 (TREMREL: 17, Last annotation update)
DE MACROPHAGE ACTIVATING LIPOPROTEIN-403 PRECURSOR.
GN MALP.
OS Mycoplasma fermentans.
OC Bacteria; Firmicutes; Bacillus/Clustidium group; Mollicutes.
MC Mycoplasmataceae; Mycoplasma.
CX NCBI_TaxID: 2115.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN K7;
RX MEDLINE 99115554; PubMed 9916088;
RA Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
RT "Differential posttranslational processing confers intraspecies
  variation of a major surface lipoprotein and a macrophage-activating
  lipopeptide of Mycoplasma fermentans.";
  EMBL: AF099215; AAD16397.1;
  FJ InterPro: IPR003760; Bmp.
  DR Pfam: PF02608; Bmp; 1.
  KW Signal; Lipoprotein.
  FT SIGNAL 1 24 POTENTIAL.
  FT CHAIN 25 428 MACROPHAGE ACTIVATING LIPOPROTEIN 403.
  SQ SEQUENCE 428 AA: 47875 MW: 57454.640 kDa pI: 5.64;

Query Match 99.48; Score 2174; DB 2; Length 428;
Best local Similarity 99.48; Pred. No. 120-117;
Matches 425; Conservative 1; Mismatches 0; Gaps 0;

QY 1 MKRSKKILLGLSPFAALLFAVAVSGNNNESNISSEKFIKSYTTINANGKQVKNNAELL 60
  |||
DB 1 MKRSKKILLGLSPFAALLFAVAVSGNNNESNISSEKFIKSYTTINANGKQVKNNAELL 60
QY 61 KLRVILIDCKIDKSFNSAFKALKAINKQTGIEIRNVTHSSNEFSAYNSALSAGHVI 120
  |||
DB 61 KLRVILIDCKIDKSFNSAFKALKAINKQTGIEIRNVTHSSNEFSAYNSALSAGHVI 120
QY 121 WVLNGFRHQSQYVDARHFEI FPNQIFKIGTDFGLTEFKWKFYSQFNKESAFITGY 180
  |||
DB 121 WVLNGFRHQSQYVDARHFEI FPNQIFKIGTDFGLTEFKWKFYSQFNKESAFITGY 180
QY 181 ATASWISQWSESPPVVASPGGAFPCVITFNESEAFKGIYYNQKHKSSKIYHTSPVKIDS 240
  |||
DB 181 ATASWISQWSESPPVVASPGGAFPCVITFNESEAFKGIYYNQKHKSSKIYHTSPVKIDS 240

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Result	No.	Score	Query		ID	Description
			Match	Length		
1	1	220.5	10.1	657	1	Y040_MYCN
2	2	207.5	9.5	551	2	Y041_MYCN
3	3	203.5	9.3	339	1	BME4_BOR04
4	4	201.5	9.2	439	1	BME4_BOR04
5	5	196.5	9.0	325	1	BME4_BOR04
6	6	192	8.8	441	1	BME4_BOR04
7	7	187	8.5	450	1	Y0F0_BOR04
8	8	185.5	8.5	341	1	BME4_BOR04
9	9	180.5	8.1	367	1	Y041_MYCN
10	10	178.5	8.2	357	1	Y041_MYCN
11	11	169	7.7	441	1	BME4_BOR04
12	12	154	7.0	441	1	BME4_BOR04
13	13	151	6.9	666	1	Y032_MYCN
14	14	142.5	6.5	454	1	BME4_BOR04
15	15	140.5	6.4	404	1	Y302_PYAP
16	16	134.5	6.1	672	1	Y042_MYCN
17	17	130.5	6.0	454	1	Y032_MYCN
18	18	129.5	5.9	1450	1	R040_MYCN
19	19	124.5	5.6	1551	1	R040_MYCN
20	20	123.5	5.5	1561	1	Y041_MYCN
21	21	119	5.4	1605	1	Y042_MYCN
22	22	118	5.4	754	1	Y040_MYCN
23	23	117.5	5.4	1882	1	Y040_MYCN
24	24	117	5.3	747	1	Y040_MYCN
25	25	116.5	5.3	405	1	Y041_PYR04
26	26	116	5.3	562	1	R040_MYCN
27	27	114.5	5.2	1729	1	R040_MYCN
28	28	114	5.2	1321	1	Y041_MYCN
29	29	113	5.2	1311	1	Y041_MYCN
30	30	113	5.2	1301	1	Y041_MYCN
31	31	112.5	5.1	840	1	Y040_MYCN
32	32	112.5	5.1	445	1	Y040_MYCN
33	33	112.5	5.1	1630	1	Y040_MYCN


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RX MEDLINE 94327986; PubMed=8050720;
RA Simpson W, Gellera W, Gellera M, Barlow A, Gellera M, Gellera M.
RI "Nucleotide sequence and analysis of the gene in Borrelia burgdorferi
R1 encoding the immunodominant P39 antigen."
RC FEMS Microbiol. Lett. 119:381-388(1994).
RN 12.
RP SEQUENCE FROM N.A.
RX MEDLINE 97132632; PubMed=8478084;
RA Aron L, Tschopp G, Gellera W, Gellera M, Gellera M, Gellera M.
RI "Identification and mapping of a chromosomal gene cluster of Borrelia
R1 burgdorferi containing genes expressed in vivo."
RC FEMS Microbiol. Lett. 145:409-414(1996).
RN 13.
RP SEQUENCE FROM N.A.
RX MEDLINE 97065943; PubMed=9403685;
RA Fraser W, Gellera W, Gellera M, Gellera M, Gellera M, Gellera M.
RA Lathrop R, White G, Ketchum K, Johnson R, Hickoy R, Gwin M,
RA DeBorja R, Gellera W, Gellera M, Gellera M, Gellera M, Gellera M.
RA Peterson J, Kottavay A, Quackenbush J, Salzberg S, Hanson M,
RA van Vleet R, Palmer N, Adams M, Gervayne J, Weidman J,
RA Osterback T, Walthery L, McDonald L, Artlich P, Bowman G,
RA Smith H, Venter J, Gellera W, Gellera M, Gellera M, Gellera M,
RA "Genomic sequence of a Lyme disease spirochaete, Borrelia
R1 burgdorferi."
RC Nature 390:580-585(1997).
RN 14.
RP SEQUENCE OF 249-339 FROM N.A.
RX MEDLINE 96111614; PubMed=7912443;
RA Ojima C, Davidson B, Saint-Girons I, Old L.
RI "Conservation of gene arrangement and an unusual organization of rRNA
R1 genes in the linear chromosomes of the Lyme disease spirochaetes
R1 Borrelia burgdorferi, B. garinii and B. azetellii."
RC Microbiology 140:2941-2940(1994).
CC -1- FUNCTION: NOT KNOWN. IMMUNOGENIC PROTEIN.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (PROBABLY).
CC -1- SIMILARITY: BELONGS TO THE BMD FAMILY OF LIPOPROTEINS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement. See http://www.ebi.ac.uk/seqdb
CC or send an email to license@ebi.ac.uk.
CC
DR EMBL: L21151; AAC72475.1;
DR EMBL: 049998; AAC44712.1;
DR EMBL: AF00114; AAC67875.1;
DR EMBL: L45050; AAC41401.1;
DR F1: B04843;
DR InterPro: IPR004760; Bmp.
DR Pfam: PF04606; Bmp; 1;
DR PROSITE: PS00013; PROFAF_LIPID-PROT; 1;
KW Antigen; Membrane; Lipoprotein; Signal; Complete proteome.
FT SIGNAL: 1 17 PROBABLY.
FT CHAIN: 18 335 BASIC MEMBRANE PROTEIN A.
FT LIPID: 18 18 N-ACYL DIPEPTIDE (PROBABLY).
FT VARIANT: 278 278 F S S (IN STRAIN 267).
SV SEQUENCE 339 AA: 46968 MW: A9581868CA70B924 CAC64;

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Query Match 9.39; Score 203; DB 1; Length 339;
Best local similarity: 24.78; Pos: 6; Len: 24;
Matches 94; Conservative 56; Mismatches 147; Indels 80; Gaps 15;

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QY 57 AELLFPEVLTEDQPTTFDSFYSATATATATPPTTITINWTSN FTAYRALS 115
115 115 115 115 115 115 115 115 115 115 115 115 115 115 115
26 SEFFVSLT GDTFDESEALNMFVVFLETFEALVLESFNSGSDLLTLD 83

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FI SIGNAL      I   13          PROBABLE.
F1 CHAIN       14    350        HYPOTHEETICAL LIPIDPROTEIN YUEN.
F1 LIPID       14              N-ACYL DIGLYCERIDE (PROBABLE).
SQ SEQUENC-I   49 AA.  47349 MW. 165517AA5A94284 CRG64;

Query Match           8.5%; Score 187; DB 1; Length 450;
Best Local Similarity 22.4%; Pred.No. 6.5E+05;
Matches 93; Conservative 61; Mismatches 145; Indels 116; Gaps 17;

QY 24 QNNDKEDKDFVLLDLEELIIMARPLEVEVALPELVLELFEPITPTPLSAFAS
DB | ||| |||| |||| | | |||| ||||| |||||
   13 AVGNSEKLGLHLSKH - PLVAVVLGVAVILPFLRANAM 51

QY 94 ELKAIRNGVDTHN - - - - NVDSNRGEATVRCALSGDHRLWLR 124
DB | ||| || ||| | | | | | | | | | | | | | |
   52 ERIQAEREDEKEECYDLSESALA PLGLAEMLCALCY 95

QY 125 GRPHGSIFPVIAAFELLERPFITLTDTIVFYVSIGPIRESATTTCVAFAF 184
DB | ||| || | | | | || || || || | | | | | |
   100 GTEMSLSELAG - QRRLADLAAGVELRN VASTTTRGGELTVSAAA 150

QY 185 WISIKGLEEAVALLEGALCVLPGRAPVTTPVHPSPFTPSVFSTATA 214
DB | | | | | | | | | | | | | | | | | | | |
   151 TLSSSKAK LTFVLMSEHLFEFFVEDNAVREFAVVAYAGCHIFAACVZAI 209

QY 245 CLKMRIVNNVISSTPAVKRVHVHILEVA-FATLITVCAMELG - AVGVMSLD 258
DB | | | | | | | | | | | | | | | | | | | |
   207 AMSM-----YKSNVAIVHS AATGICVI DASHNEKEPKRWVGWKRY 255

QY 299 LGDIQ-LKPDPQLSVLEHKFGAVALLILLEREGDLEVVLREFAREWS 346
DB | | | | | | | | | | | | | | | | | | | |
   256 ASQVLEHHHTVTSNKVAN - TVVERV VEEKALGRTTESCLL 309

QY 350 HESTLGFPGVVAERHH-SHLLTGAFASP - FAKPQESKGLGPRVINS-DNAIF 404
DB | | | | | | | | | | | | | | | | | | | |
   299 TGLAQD-QVGLSPSKQNLSDVTKAVRKRFTHDELIPA-----TERAPIK 345

RESULT 8
BMVB_BORAF BORAF STANLARD; PRD; 41 AA.
ID 031284;
DI 15 DEC-1998 (Ref. 37; Created)
DT 15-DEC-1998 (Ref. 37; last sequence update)
DE 15 DEC-1998 (Ref. 37; last annotation update)
CN Basic membrane protein B precursor.
OS Borrelia atzevii.
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
RX Ref_TaxID_29512.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PKO7.
KW MEDLINE: 98010210; PubMed: 9450727;
RA Roessler D.; Hauser U.; Wihske B.;
RT "Heterogeneity of BorA (P49) among European isolates of Borrelia burgdorferi sensu lato and influence of interspecies variability on sero-diagnosis."
KT J. Clin. Microbiol., 35(27):2752-2758(1997).
KC C-1 SUBCELLULAR LOCALIZATION. Attached to the membrane by a lipid anchor (Probable).
CC C-1 SIMILARITY. BELONGS TO THE BMF FAMILY OF LIPID-PROTEINS.
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CC PRC: X81519; CAA57249.1.

```


031362;
 DT 15-DEC-1998 (Rel. 37, Created)
 DI 15-DEC-1998 (Rel. 37, Last sequence update)
 DI 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Basic membrane protein B precursor.
 GN BMBP.
 OS Borrelia burgdorferi.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_taxid:29519;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN P81;
 RX MEDLINE:98010210; PubMed:9450727;
 RA Roessler B., Bauser B., Wilske B.,
 RT "Heretofore, only of BapA (239) among European isolates of Borrelia
 RT burgdorferi sensu lato and influence of interspecies variability on
 RT serodiagnosis."
 RI J. Clin. Microbiol. 45:2752-2758(1997).
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
 (Probable).
 CC -1- SIMILARITY: BELONGS TO THE BMP FAMILY OF LIPOPROTEINS.
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 CC or send an email to license@sib-sib.ch.
 DE EMBL: X81518; CAA57248.1;
 DR InterPro: IPR003760; Bmp.
 DR Pfam: PF02699; Bmp_1.
 DR ProSITE: PS00018; PROKAR_LIPOPROTEIN; 1.
 KW Membrane; Lipoprotein; Signal.
 FT SIGNAL 1 14 PROBABLE.
 FT CHAIN 15 44 BASIC MEMBRANE PROTEIN B.
 FT LIPID 15 15 N-ACYL DIGLYCERIDE (PROBABLE).
 SQ SEQUENCE 341 AA: 37246 MW: 44280 PREDICTED C9A CR664;

Query Match 7.78; Score 169; DB 1; Length 341;
 Best Local Similarity 21.58; Pred. No. 0.0084;
 Matches 92; Conservative 92; Mismatches 169; Indels 80; Gaps 15;
 QY 17 TIPAAVAV...GRHSNHLRFLELLEFVLT...GAGAEAVNDELLEFVLT...74
 DB 7 TEGHLLSTAGNTERSSS-----KIKSLMVDGVLD 49
 QY 75 DESTRGAEALAKAPKAGLLLRNVLEAGHESAYKSALESWIKIWLKPE 127
 DB 40 DKSTSSAREALKEELFELNTERVSSAAEVSYSSTIRIKRSGELWLVGYND 99
 QY 129 EQQTEKLVLAHHRTGEPDRTKTDIDPTDEYKWEVSLNIPESATVYALIA 183
 DB 100 TDASLS-----VSLNPKSLVGLIDVYSVAVQIPKMLGVPRIPQCAFLADYIAA 151
 QY 184 SWESLLESEKLVANAGSALGV...HILHRAELGVYHDEKSKINYESEVELLS 213
 DB 152 EASVSEFLLELSEAVSEAVALEFTLACAVASAV...VLSVSGV...VAVH 203
 QY 241 GTTAEKWRVIRVSVSSITANKYRIHVTLVAGVATHTVRLANKGVYGVGVSDQM 400
 DB 204 GPALANRYAPALHLL-----HPMAVAGVSEVFAHTT...GVYVVSAGVAGVGR 252
 QY 401 LQDKRHLVSWIKHKGAVYVTLIDLEFF...EYKPVVWVVKAKKWSHFEQKPKW 358
 DB 253 LAPEN...FIVSVKGVVALVTSVSEVIRKHNWLEK...TGGQELGVVGLSHANZPEY 409
 QY 409 GVAVRHRTTETAKINRE...PEATEK 385
 DB 410 LVTERKIVNEELIVPNHGVSEVETKQIKL 441

RESULT 12
 BMBP_BORBU
 ID BMBP_BORBU STANDARD: PRT: 441 AA.
 AC 044743;
 DI 15-DEC-1998 (Rel. 37, Created)
 DI 15-DEC-1998 (Rel. 37, Last sequence update)
 DI 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Basic membrane protein B precursor.
 GN BMBP OR BHO385.
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_taxid:139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN J01;
 RX MEDLINE:96178617; PubMed:8606088;
 RA Ramamoorthy R., Pevsnel L., Philipp M.T.;
 RI "Molecular characterization, genomic arrangement, and expression of
 RI bmbp, a new member of the bmp class of genes encoding membrane
 RI proteins of Borrelia burgdorferi."
 RI Infect. Immun. 64:1259-1264(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN A103 35710 / B31;
 RX MEDLINE:98065943; PubMed 9403685;
 RA Fraser C.M., Gasjics S., Huang W.M., Sutton G.G., Clayton R.A.,
 RA Catharta E., White G., Kotchen K.A., Dodson R., Blakes E.K., Gwin M.,
 RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Hanson M.,
 RA Peterson J., Korfava A.R., Quackenbush J., Salzberg S., Henson M.,
 RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman C.,
 RA Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
 RA Garland S., Fujii C., Cotton M.D., Heist K., Roberts K., Hatch R.,
 RA Smith B.O., Venter J.C.;
 RI "Genomic sequence of a Lyme disease spirochete, Borrelia
 RI burgdorferi."
 RI Nature 393:590-594(1997).
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
 (Probable).
 CC -1- SIMILARITY: BELONGS TO THE BMP FAMILY OF LIPOPROTEINS.
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 CC entities requires a license agreement (see <http://www.isb-sib.ch>)
 CC or send an email to license@sib-sib.ch.
 DE EMBL: 045450; AAC13984.1;
 DR EMBL: AK001144; AAB91505.1;
 DR TIGR: BHO385;
 DR InterPro: IPR003760; Bmp.
 DR Pfam: PF02699; Bmp_1.
 DR ProSITE: PS00018; PROKAR_LIPOPROTEIN; 1.
 KW Membrane; Lipoprotein; Signal; Complete proteome.
 FT SIGNAL 1 16 PROBABLE.
 FT CHAIN 1 43 BASIC MEMBRANE PROTEIN B.
 FT LIPID 17 17 N-ACYL DIGLYCERIDE (PROBABLE).
 SQ SEQUENCE 411 AA: 47163 MW: 64666 PREDICTED C9A CR664;

Query Match 7.08; Score 154; DB 1; Length 341;
 Best Local Similarity 23.28; Pred. No. 0.0074;
 Matches 92; Conservative 92; Mismatches 152; Indels 98; Gaps 20;
 QY 22 VSGNRSNEMETKEKTSKYL...GAEFGVAVFNAELTFVFI...EPTKTPKPEKSA 92
 DB 15 VAGSSSD...-----GSEAKTV...341
 QY 84 PEALKATKQGLIEIRVSVSS...SEATSSALASAKRIWLNKPEKPEK 142
 DB 46 SKATKRLKAGDNG...LGRASIGREYLGAGLEL...341
 DB 46 SKATKRLKAGDNG...LGRASIGREYLGAGLEL...341

GenCore version 4.5
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OM protein protein search, using sw model

Run on: July 23, 2002, 11:20:17, Search time 20:47:35 seconds
(without alignments)
1970.561 Million cell updates/sec

Title: US-09-601-371_2

Perfect score: 2189

Sequence: 1 MFPEFFHLLSLFAMILFA.....HNVSEGLA:LSALNPAAE 129

Scoring table:

BLSDM62

Gapop 10.0, Gapext 0.5

Searched: 284138 seqs, 9608934 residues

Total number of hits satisfying chosen parameters: 284148

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR-71:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	462	21.1	461	2	Protein
2	225	10.4	450	2	G95097
3	220.5	10.1	667	2	hypothetical protein
4	213	9.7	474	2	conserved hypothetical
5	207.5	9.5	591	2	membrane protein
6	204.5	9.3	525	2	G92914
7	203	9.3	439	2	F75147
8	201.5	9.2	357	2	D96986
9	198.5	9.1	375	2	H77318
10	197	9.0	441	2	F70147
11	192	8.9	350	2	F86891
12	190.5	8.7	524	2	D82944
13	187	8.5	350	1	C92609
14	180.5	8.2	357	2	A01248
15	178.5	8.2	357	2	A31510
16	173	7.9	459	2	F72418
17	155.5	7.1	360	2	H75157
18	153	7.0	337	2	B97374
19	153	7.0	337	2	A35591
20	152	6.9	470	2	A72494
21	151	6.9	665	1	D61203
22	144	6.6	322	2	F84246
23	143.5	6.5	353	2	G75147
24	140.5	6.4	494	2	G75161
25	138	6.3	624	2	F25089
26	137	6.3	539	2	D82886
27	136.5	6.2	1225	2	G53591
28	134.5	6.1	805	2	G82884
29	134.5	6.1	2451	2	I29679

ALIGNMENTS

RESULTS

1

Protein

Protein

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1. The first part of the document discusses the importance of maintaining accurate records of all transactions and activities. It emphasizes that proper record-keeping is essential for transparency and accountability, particularly in financial matters. The text suggests that organizations should implement robust systems to track and document every aspect of their operations, from procurement to sales.

2. The second part of the document addresses the challenges of data management in a rapidly changing environment. It highlights the need for flexible and scalable solutions that can adapt to evolving requirements. The author argues that investing in modern data infrastructure is crucial for ensuring that information remains relevant and accessible over time.

3. The third part of the document explores the role of technology in enhancing operational efficiency. It discusses various tools and platforms that can streamline processes, reduce errors, and improve overall productivity. The text encourages organizations to embrace digital transformation and leverage technology to gain a competitive edge.

4. The fourth part of the document focuses on the importance of collaboration and communication within an organization. It stresses that effective teamwork and clear communication channels are vital for achieving common goals and resolving issues promptly. The author suggests that fostering a culture of openness and collaboration can lead to better outcomes and higher employee satisfaction.

5. The fifth part of the document discusses the need for continuous learning and development. It emphasizes that in a fast-paced world, individuals and organizations must stay updated with the latest trends and technologies. The text encourages investing in training and development programs to ensure that the workforce is equipped with the skills needed for future success.

6. The sixth part of the document addresses the importance of risk management and compliance. It highlights that organizations must proactively identify and mitigate potential risks to avoid legal and financial repercussions. The text suggests implementing comprehensive risk management frameworks and staying up-to-date with regulatory requirements.

7. The seventh part of the document discusses the role of leadership in driving organizational success. It emphasizes that strong leaders are essential for setting a clear vision, inspiring teams, and making strategic decisions. The author suggests that leaders should focus on building trust, fostering innovation, and ensuring that the organization's values are reflected in its actions.

8. The eighth part of the document addresses the importance of sustainability and social responsibility. It highlights that organizations have a responsibility to their stakeholders beyond just financial performance. The text suggests integrating sustainability into the core business strategy and reporting on social and environmental impacts.

9. The ninth part of the document discusses the importance of customer satisfaction and loyalty. It emphasizes that providing excellent customer service is a key differentiator for many organizations. The text suggests implementing feedback loops and personalized experiences to enhance customer engagement and retention.

10. The tenth part of the document concludes by summarizing the key points discussed and offering final thoughts on the future of business. It emphasizes that success in the modern era requires a combination of strategic vision, operational excellence, and a commitment to continuous improvement. The author encourages organizations to stay resilient and adaptable in the face of uncertainty.

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OM protein protein search, using sw model

Run on: July 23, 2002, 14:29:42 : Search time 11.56 seconds
(without alignments)
1506,801 Million cell updates/sec

Title: US-09-601-371-2
Perfect score: 2189
Sequence: 1 MEKSKKELLLKLSF-AALVLA.....LAV:KELIA:LAIRAAK 429

Scoring table: B0/SUM62
Gapop 10.0 : Gapext 0.5

Searched: 747574 seqs, 11107796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listed first 45 summaries

Database : A_GenSeq_032802:*

Rank	Seq ID	Score	Length	DB ID	Description
1	11107796	2189	429	AAK5432	Inflammatory cytokine
2	11107796	2092	429	AAW2272	Interleukin 10
3	11107796	1966	429	AAK5432	Interleukin 10
4	11107796	1941	453	AAK4086	4 kb reduplication as
5	11107796	1844	448	AAK93343	Gene encoding the
6	11107796	1834	442	AAK67582	Cancer metastasis
7	11107796	1834	451	AAK01855	Myeloplasma hyphen
8	11107796	1648	424	AAK01860	Propionibacterium
9	11107796	1552	429	AAK93289	Streptococcus pneumoniae
10	11107796	1552	351	AAK81632	Streptococcus pneumoniae
11	11107796	1552	328	AAW56066	Streptococcus pneumoniae

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2189	100.0	429	AAK5432	Inflammatory cytokine
2	2092	95.4	429	AAW2272	Interleukin 10
3	1966	89.7	429	AAK5432	Interleukin 10
4	1941	86.8	453	AAK4086	4 kb reduplication as
5	1844	81.9	448	AAK93343	Gene encoding the
6	1834	79.5	442	AAK67582	Cancer metastasis
7	1834	79.5	451	AAK01855	Myeloplasma hyphen
8	1648	66.8	424	AAK01860	Propionibacterium
9	1552	59.2	429	AAK93289	Streptococcus pneumoniae
10	1552	59.2	351	AAK81632	Streptococcus pneumoniae
11	1552	59.2	328	AAW56066	Streptococcus pneumoniae

12	204.5	54.8	440	34	AAK5432	Interleukin 10
13	204.5	54.8	424	20	AAK5432	Interleukin 10
14	204.5	54.8	424	20	AAK5432	Interleukin 10
15	204.5	54.8	424	20	AAK5432	Interleukin 10
16	196.5	54.8	424	20	AAK5432	Interleukin 10
17	196.5	54.8	424	20	AAK5432	Interleukin 10
18	196.5	54.8	424	20	AAK5432	Interleukin 10
19	196.5	54.8	424	20	AAK5432	Interleukin 10
20	196.5	54.8	424	20	AAK5432	Interleukin 10
21	196.5	54.8	424	20	AAK5432	Interleukin 10
22	196.5	54.8	424	20	AAK5432	Interleukin 10
23	196.5	54.8	424	20	AAK5432	Interleukin 10
24	196.5	54.8	424	20	AAK5432	Interleukin 10
25	196.5	54.8	424	20	AAK5432	Interleukin 10
26	196.5	54.8	424	20	AAK5432	Interleukin 10
27	196.5	54.8	424	20	AAK5432	Interleukin 10
28	196.5	54.8	424	20	AAK5432	Interleukin 10
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30	196.5	54.8	424	20	AAK5432	Interleukin 10
31	196.5	54.8	424	20	AAK5432	Interleukin 10
32	196.5	54.8	424	20	AAK5432	Interleukin 10
33	196.5	54.8	424	20	AAK5432	Interleukin 10
34	196.5	54.8	424	20	AAK5432	Interleukin 10
35	196.5	54.8	424	20	AAK5432	Interleukin 10
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37	196.5	54.8	424	20	AAK5432	Interleukin 10
38	196.5	54.8	424	20	AAK5432	Interleukin 10
39	196.5	54.8	424	20	AAK5432	Interleukin 10
40	196.5	54.8	424	20	AAK5432	Interleukin 10
41	196.5	54.8	424	20	AAK5432	Interleukin 10
42	196.5	54.8	424	20	AAK5432	Interleukin 10
43	196.5	54.8	424	20	AAK5432	Interleukin 10
44	196.5	54.8	424	20	AAK5432	Interleukin 10
45	196.5	54.8	424	20	AAK5432	Interleukin 10

COMMENTS

RESULT 1
AAK5432

AAK5432

AAK5432

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AAK5432

PI New antigenic proteins from Borrelia burgdorferi useful in vaccines
PI for raising antibodies or for diagnostic detection of specific
PI antibodies
PS Claim 1: Columns 29-32: 3pp; English.
XX This represents the Borrelia burgdorferi antigenic protein p39 alpha
XX which is immunoreactive with mammalian Lyme borreliosis serum. The
XX Borrelia antigenic proteins p39 alpha and p39 beta are used in vaccines
XX to protect against Lyme disease, as assay reagents to detect specific
XX antibodies in the serum (diagnostic of Lyme disease), and to raise
XX antibodies, either for diagnosis (by detecting the corresponding antigen)
XX or in screening agents for ability to inhibit expression of the protein.

XX Sequence 339 AA;

Query Match 9.99; Score 2044; bp 19; Length 339;
Best Local Similarity 24.7%; Pred. No. 1.7e-07;
Matches 93; Conservative 56; Mismatches 117; Indels 80; Gaps 15;
QY 57 APLLEFTEVITLDEPDEGSEKALFALEDAEDGDTIDRAVLEEN EFAYVSAIS 115
31 11 31 11 11 11 11 31 31 11 31 11 11 11 11 11 11 11 11
DB 26 scipphslii iiiiibbbscscslg iiiiikiiibssssyisdliaiiid 92
QY 116 AAKIKWVNPWQGGKQVYVAKETTERGQVLTG TQTHYVWYSLQINPE 173
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 86 dsidliiqllytisdpy iiiiipdekyttdiplysdipspoloptrape 136
QY 174 SAPTEVYALAWCTDQPPPEVAVSISZAFVAVVDFVDAVYVDEPFPSRYVH 233
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 137 iiiiifjv iiiiisv iiii iiii iiii iiii iiii iiii iiii iiii 156
QY 234 SVKLSSCTAEKRN.VIRNVLSTLADVYKSHVLSVADATVETVELANKQYVIG 293
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 192 STGLEHRSCTLLSSGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSL 246
QY 294 VSSGEMLTETLFTLLSFLKIKLAAVETLLEKTLLEKLEAVVAVVEKAEPSHRE 353
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 241 iiiiidpyv iiiiidpyv iiii iiii iiii iiii iiii iiii iiii iiii 309
QY 356 QPRWLVVAPRQVADIIQVAFIRPPLAIVQVVFVAVVAVVAVVAVVAVVAV 411
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 269 iiii iiii iiii iiii iiii iiii iiii iiii iiii iiii iiii 312
QY 412 VSEPTLPAITLAINE 425
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 313 iiii iiii iiii iiii iiii iiii iiii iiii iiii iiii iiii 359
RESULT 15
AAV19984
ID AAV19984 standard; Protein: 339 AA.
XX AAV19984;
AC AAV19984;
XX 19 JUL-1999 (first entry)
XX 19 JUL-1999 (first entry)
DE B. burgdorferi antigenic protein, p541aa.
XX Antigenic protein; vaccine; Lyme disease; infection; detection.
XX Borrelia burgdorferi.
XX W0905071-A1.
XX 30-06-1998.
XX 18-JUN-1998; 98W0-0512718.
XX 04-SEP-1997; 97US-0057483.
XX 20 JUN-1997; 97US-0050359.
XX 22-JUL-1997; 97US-0053444.

PK 22-JUL-1997; 97US-0053477.
XX (HUMA-) HUMAN GENOME SCI INC.
PA (MED-) MEDIMUNE INC.
XX Choi GH, Erwin AL, Hanson MS, Rathbun R;
XX WPL: 1993-189980/16.
XX N ISDH: AAX61681.
XX New isolated Borrelia burgdorferi nucleic acids used to develop
XX products for the diagnosis, prevention and treatment of diseases
XX caused by Borrelia, particularly Lyme disease
XX Claim 12: Page 149-150; 275pp; English.
XX This sequence represents a Borrelia burgdorferi (BB) protein of the
XX invention, which is suitable for use in a vaccine. The BB polypeptides
XX can be used in vaccines for eliciting protective antibodies to members of
XX the Borrelia genus, particularly for the use against Lyme disease in
XX humans and animals. They can be used for prevention or attenuating an
XX infection caused by a member of the Borrelia genus. The protein can also
XX be used for detection of members of the Borrelia genus.
XX Sequence 339 AA;
Query Match 9.99; Score 2044; bp 20; Length 339;
Best Local Similarity 24.7%; Pred. No. 1.7e-07;
Matches 93; Conservative 56; Mismatches 117; Indels 80; Gaps 15;
QY 57 APLLEFTEVITLDEPDEGSEKALFALEDAEDGDTIDRAVLEEN EFAYVSAIS 115
31 11 31 11 11 11 11 31 31 11 31 11 11 11 11 11 11 11 11
DB 26 scipphslii iiiiibbbscscslg iiiiikiiibssssyisdliaiiid 92
QY 116 AAKIKWVNPWQGGKQVYVAKETTERGQVLTG TQTHYVWYSLQINPE 173
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 86 dsidliiqllytisdpy iiiiipdekyttdiplysdipspoloptrape 136
QY 174 SAPTEVYALAWCTDQPPPEVAVSISZAFVAVVDFVDAVYVDEPFPSRYVH 233
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 137 iiiiifjv iiiiisv iiii iiii iiii iiii iiii iiii iiii iiii 156
QY 234 SVKLSSCTAEKRN.VIRNVLSTLADVYKSHVLSVADATVETVELANKQYVIG 293
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 192 STGLEHRSCTLLSSGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSL 246
QY 294 VSSGEMLTETLFTLLSFLKIKLAAVETLLEKTLLEKLEAVVAVVEKAEPSHRE 353
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 241 iiiiidpyv iiiiidpyv iiii iiii iiii iiii iiii iiii iiii iiii 309
QY 356 QPRWLVVAPRQVADIIQVAFIRPPLAIVQVVFVAVVAVVAVVAVVAVVAV 411
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DB 269 iiii iiii iiii iiii iiii iiii iiii iiii iiii iiii iiii 312
QY 412 VSEPTLPAITLAINE 425
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DB 313 iiii iiii iiii iiii iiii iiii iiii iiii iiii iiii iiii 359
RESULT 15
AAV19984
ID AAV19984 standard; Protein: 339 AA.
XX AAV19984;
AC AAV19984;
XX 19 JUL-1999 (first entry)
XX 19 JUL-1999 (first entry)
DE B. burgdorferi antigenic protein, p541aa.
XX Antigenic protein; vaccine; Lyme disease; infection; detection.
XX Borrelia burgdorferi.
XX W0905071-A1.
XX 30-06-1998.
XX 18-JUN-1998; 98W0-0512718.
XX 04-SEP-1997; 97US-0057483.
XX 20 JUN-1997; 97US-0050359.
XX 22-JUL-1997; 97US-0053444.

Search completed: July 23, 2002, 14:32:18
Job time: 166 sec